

Team 8
CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/785,455

CRF Processing Date: 2/21/99
Edited by: HC
Verified by: HC (STIC staff)

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically: ENTERED #2

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included: _____

Deleted extra invalid, headings used by an applicant, specifically: "APPLICANT" _____

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically: _____

Corrected an obvious error in the response, specifically: _____

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically: _____

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

Other: added (B) FILING DATE, heading under (vi) CURRENT APPLICATION DATA, _____

* Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/785,455.DATE: 02/21/97
TIME: 15:30:00

INPUT SET: S15668.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT
6 (A) NAME: Hodgson, John
7 (B) STREET: Great West Road
8 (C) CITY: Brentford
9 (D) STATE OR PROVINCE: Middlesex
10 (E) COUNTRY: United Kingdom
11 (F) POSTAL CODE: TW8 9EP
12
13 APPLICANT
14 (A) NAME: Hodgson, John
15 (B) STREET: Great West Road
16 (C) CITY: Brentford
17 (D) STATE OR PROVINCE: Middlesex
18 (E) COUNTRY: United Kingdom
19 (F) POSTAL CODE: TW8 9EP
20
21 (ii) TITLE OF THE INVENTION: Novel tRNA Synthetase
22
23
24 (iii) NUMBER OF SEQUENCES: 2
25
26 (iv) COMPUTER-READABLE FORM:
27 (A) MEDIUM TYPE: Diskette
28 (B) COMPUTER: IBM Compatible
29 (C) OPERATING SYSTEM: DOS
30 (D) SOFTWARE: FastSEQ for Windows Version 2.0
31
32 (v) CURRENT APPLICATION DATA:
33 (A) APPLICATION NUMBER:
34 (B) FILING DATE:
35 (2) INFORMATION FOR SEQ ID NO:1:
36
37 (i) SEQUENCE CHARACTERISTICS:
38 (A) LENGTH: 1974 base pairs
39 (B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
41 (D) TOPOLOGY: linear
42
43 (ii) MOLECULE TYPE: Genomic DNA
44
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
46

Does Not Comply
Corrected Diskette Needed

INPUT SET: S15668.raw

47	ATGGCTAAAG	AAACATTTA	TATAACAACC	CCAATATACT	ATCCTAGTGG	GAATTACAT	60
48	ATAGGACATG	CATATTCTAC	AGTGGCTGGA	GATGTTATTG	CAAGATATAA	GAGAATGCAA	120
49	GGATATGATG	TTCGTTATTT	GAAGTAAAGAC	GATGAAACACG	GTCAAAAAAT	TCAAGAAAAA	180
50	GCTAAAAAG	CTGGTAAGAC	AGAAAATTGAA	TATTTGGATG	AGATGATTGC	TGGAATTAAA	240
51	CAATTGTGGG	CTAAGCTTGA	AATTCAAAT	GATGATTTTA	TCAGAACAC	TGAAGAACGT	300
52	CATAAACATG	TCGTTGAGCA	AGTGGTTGAA	CGTTTATTAA	AGCAAGGTGA	TATCTATTAA	360
53	GGTGAATATG	AAGGTTGGTA	TTCTGTTCCG	GATGAAACAT	ACTATACAGA	GTCACAATT	420
54	GTAGACCCAC	AATACGAAAA	CGGTAAGGAA	ATTGGTGGCA	AAAGTCCAGA	TTCTGGACAC	480
55	GAAGTTGAAC	TAGTTAAAGA	AGAAAAGTTAT	TTCTTTAATA	TTAGTAAATA	TACAGACCGT	540
56	TTATTAGAGT	TCTATGACCA	AAATCCAGAT	TTTATACAAAC	CACCATCAAG	AAAAAAATGAA	600
57	ATGATTAACA	ACTTCATTA	ACCAAGGACTT	GCTGATTTAG	CTGTTCTCG	TACATCATT	660
58	AACTGGGGTG	TCCATGTTCC	GTCTAATCCA	AAACATGTTG	TTTATGTTG	GATTGATGCG	720
59	TTAGTTAACT	ATATTCAGC	ATTAGGCTAT	TTATCAGATG	ATGAGTCACT	ATTTAACAAA	780
60	TACTGGCCAG	CAGATATTCA	TTTAATGGCT	AAGGAAATTG	TGCGATTCCA	CTCAATTATT	840
61	TGGCCTATT	TATTGATGGC	ATTAGACTTA	CCGTTACCTA	AAAAAGTCTT	TGCACATGGT	900
62	TGGATTTGA	TGAAAGATGG	AAAAATGAGT	AAATCTAAAG	GTAATGTTGT	AGACCCCTAA	960
63	ATTTAATTG	ATCGCTATGG	TTTAGATGCT	ACACGTTATT	ATCTAATGCG	TGAATTACCA	1020
64	TTGGGTTCA	ATGGCGTATT	TACACCTGAA	GCATTGTTG	ACCGTACAAA	TTTCGATCTA	1080
65	GCAAATGACT	TAGGTAACCT	AGTAAACCGT	ACGATTCTA	TGTTAATAA	GTACTTTGAT	1140
66	GGCGAATTAC	CAGCGTATCA	AGGTCCACTT	CATGAATTAG	ATGAAGAAAT	GGAAGCTATG	1200
67	GCTTTAGAAA	CAGTGAAAG	CTACACTGAA	AGCATGGAAA	GTTTGCAATT	TTCTGTGGCA	1260
68	TTATCTACGG	TATGGAAGTT	TATAAGTGA	ACGAATAAGT	ATATTGACGA	AACAACGCC	1320
69	TGGGTATTAG	CTAAGGACGA	TAGCCAAAAA	GATATGTTAG	GCAATGTAAT	GGCTCACTTA	1380
70	GTTGAAAATA	TTCGTTATGC	AGCTGTATTA	TTACGTCCAT	TCTTAACACA	TGCGCCGAAA	1440
71	GAGATTTTTG	AAACATTGAA	CATAAACAAAT	CCTCAATTAA	TGGAATTAG	TAGTTTAGAG	1500
72	CAATATGGT	TGCTTACTGA	GTCAATTATG	GTTACTGGC	AACCTAAACC	TATTTTCCC	1560
73	AGATTGGATA	GCGAAGCGGA	AATTGCATAT	ATCAAAGAAAT	CAATGCAACC	GCCTGCTACT	1620
74	GAAGAGGAAA	AAGAAGAGAT	TCCTAGAAA	CCTCAAATTG	ATATTAAAGA	CTTTGATAAA	1680
75	GTTGAAATT	AGGCAGCAAC	GATTATTGAT	GCTGAACATG	TTAAGAAGTC	AGATAAGCTT	1740
76	TTAAAAATT	AAAGTAGACTT	AGATTCTGAA	CAAAGACAAA	TTGTATCAGG	AATTGCCAAA	1800
77	TTCTATACAC	CAGATGATAT	TATTGGTAA	AAAGTAGCAG	TTGTTACTAA	CCTGAAACCA	1860
78	GCTAAATTAA	TGGGACAAAAA	ATCTGAAGGT	ATGATATTAT	CTGCTGAAAAA	AGATGGTGT	1920
79	TTAACCTTAG	TAAGTTTAC	AAAGTGAATT	CCAAATGGT	CAGTGATTAA	ATAA	1974

80
81 (2) INFORMATION FOR SEQ ID NO:2:
82

83 (i) SEQUENCE CHARACTERISTICS:
84 (A) LENGTH: 657 amino acids
85 (B) TYPE: amino acid
86 (C) STRANDEDNESS: single
87 (D) TOPOLOGY: linear

88 (ii) MOLECULE TYPE: peptide

89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

93	Met	Ala	Lys	Glu	Thr	Phe	Tyr	Ile	Thr	Thr	Pro	Ile	Tyr	Tyr	Pro	Ser
94	1			5				10				15				
95	Gly	Asn	Leu	His	Ile	Gly	His	Ala	Tyr	Ser	Thr	Val	Ala	Gly	Asp	Val
96					20				25			30				
97	Ile	Ala	Arg	Tyr	Lys	Arg	Met	Gln	Gly	Tyr	Asp	Val	Arg	Tyr	Leu	Thr
98					35			40			45					
99	Gly	Thr	Asp	Glu	His	Gly	Gln	Lys	Ile	Gln	Glu	Lys	Ala	Gln	Lys	Ala

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/785,455DATE: 02/21/97
TIME: 15:30:07

INPUT SET: S15668.raw

100 50 55 60
101 Gly Lys Thr Glu Ile Glu Tyr Leu Asp Glu Met Ile Ala Gly Ile Lys
102 65 70 75 80
103 Gln Leu Trp Ala Lys Leu Glu Ile Ser Asn Asp Asp Phe Ile Arg Thr
104 85 90 95
105 Thr Glu Glu Arg His Lys His Val Val Glu Gln Val Phe Glu Arg Leu
106 100 105 110
107 Leu Lys Gln Gly Asp Ile Tyr Leu Gly Glu Tyr Glu Gly Trp Tyr Ser
108 115 120 125
109 Val Pro Asp Glu Thr Tyr Tyr Thr Glu Ser Gln Leu Val Asp Pro Gln
110 130 135 140
111 Tyr Glu Asn Gly Lys Ile Ile Gly Gly Lys Ser Pro Asp Ser Gly His
112 145 150 155 160
113 Glu Val Glu Leu Val Lys Glu Glu Ser Tyr Phe Phe Asn Ile Ser Lys
114 165 170 175
115 Tyr Thr Asp Arg Leu Leu Glu Phe Tyr Asp Gln Asn Pro Asp Phe Ile
116 180 185 190
117 Gln Pro Pro Ser Arg Lys Asn Glu Met Ile Asn Asn Phe Ile Lys Pro
118 195 200 205
119 Gly Leu Ala Asp Leu Ala Val Ser Arg Thr Ser Phe Asn Trp Gly Val
120 210 215 220
121 His Val Pro Ser Asn Pro Lys His Val Val Tyr Val Trp Ile Asp Ala
122 225 230 235 240
123 Leu Val Asn Tyr Ile Ser Ala Leu Gly Tyr Leu Ser Asp Asp Glu Ser
124 245 250 255
125 Leu Phe Asn Lys Tyr Trp Pro Ala Asp Ile His Leu Met Ala Lys Glu
126 260 265 270
127 Ile Val Arg Phe His Ser Ile Ile Trp Pro Ile Leu Leu Met Ala Leu
128 275 280 285
129 Asp Leu Pro Leu Pro Lys Lys Val Phe Ala His Gly Trp Ile Leu Met
130 290 295 300
131 Lys Asp Gly Lys Met Ser Lys Ser Lys Gly Asn Val Val Asp Pro Asn
132 305 310 315 320
133 Ile Leu Ile Asp Arg Tyr Gly Leu Asp Ala Thr Arg Tyr Tyr Leu Met
134 325 330 335
135 Arg Glu Leu Pro Phe Gly Ser Asp Gly Val Phe Thr Pro Glu Ala Phe
136 340 345 350
137 Val Glu Arg Thr Asn Phe Asp Leu Ala Asn Asp Leu Gly Asn Leu Val
138 355 360 365
139 Asn Arg Thr Ile Ser Met Val Asn Lys Tyr Phe Asp Gly Glu Leu Pro
140 370 375 380
141 Ala Tyr Gln Gly Pro Leu His Glu Leu Asp Glu Glu Met Glu Ala Met
142 385 390 395 400
143 Ala Leu Glu Thr Val Lys Ser Tyr Thr Glu Ser Met Glu Ser Leu Gln
144 405 410 415
145 Phe Ser Val Ala Leu Ser Thr Val Trp Lys Phe Ile Ser Arg Thr Asn
146 420 425 430
147 Lys Tyr Ile Asp Glu Thr Thr Pro Trp Val Leu Ala Lys Asp Asp Ser
148 435 440 445
149 Gln Lys Asp Met Leu Gly Asn Val Met Ala His Leu Val Glu Asn Ile
150 450 455 460
151 Arg Tyr Ala Ala Val Leu Leu Arg Pro Phe Leu Thr His Ala Pro Lys
152 465 470 475 480

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/785,455DATE: 02/21/97
TIME: 15:30:11

INPUT SET: S15668.raw

153 Glu Ile Phe Glu Gln Leu Asn Ile Asn Asn Pro Gln Ph Met Glu Phe
154 485 490 495
155 Ser Ser Leu Glu Gln Tyr Gly Val Leu Thr Glu Ser Ile Met Val Thr
156 500 505 510
157 Gly Gln Pro Lys Pro Ile Phe Pro Arg Leu Asp Ser Glu Ala Glu Ile
158 515 520 525
159 Ala Tyr Ile Lys Glu Ser Met Gln Pro Pro Ala Thr Glu Glu Glu Lys
160 530 535 540
161 Glu Glu Ile Pro Ser Lys Pro Gln Ile Asp Ile Lys Asp Phe Asp Lys
162 545 550 555 560
163 Val Glu Ile Lys Ala Ala Thr Ile Ile Asp Ala Glu His Val Lys Lys
164 565 570 575
165 Ser Asp Lys Leu Leu Lys Ile Gln Val Asp Leu Asp Ser Glu Gln Arg
166 580 585 590
167 Gln Ile Val Ser Gly Ile Ala Lys Phe Tyr Thr Pro Asp Asp Ile Ile
168 595 600 605
169 Gly Lys Lys Val Ala Val Val Thr Asn Leu Lys Pro Ala Lys Leu Met
170 610 615 620
171 Gly Gln Lys Ser Glu Gly Met Ile Leu Ser Ala Glu Lys Asp Gly Val
172 625 630 635 640
173 Leu Thr Leu Val Ser Leu Pro Ser Ala Ile Pro Asn Gly Ala Val Ile
174 645 650 655
175 Lys
176
177